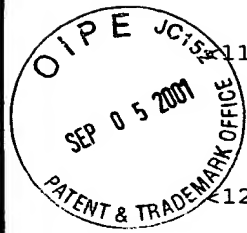


SEQUENCE LISTING



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MACALLISTER, THOMAS W.
SETHURAMAN, NATARAJAN
FREEMAN, ABBIE G.

<120> GENETICALLY ENGINEERED GLUTAMINASE AND ITS USE IN
ANTIVIRAL AND ANTICANCER THERAPY

<130> 023032/0108

<140> 09/842,628

<141> 2001-04-27

<150> 08/050,482

<151> 1995-04-25

<150> PCT/US92/10421

<151> 1992-12-04

<150> DE P 4140003.8

<151> 1991-12-04

<160> 22

<170> PatentIn Ver. 2.1

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Lys	Glu	Val	Glu	Asn	Gln	Gln	Lys	Leu	Ala	Asn	Val	Val	Ile	Leu	Ala	
1				5					10					15		

acc	ggc	ggc	acc	atc	gcc	ggc	gct	ggc	gcc	agc	gcg	gcc	aac	agc	gcc	96
Thr	Gly	Gly	Thr	Ile	Ala	Gly	Ala	Gly	Ala	Ser	Ala	Ala	Asn	Ser	Ala	
			20					25					30			

acc	tac	cag	gct	gcc	aag	gtt	ggc	gtc	gac	aag	ctg	att	gcc	ggc	gtg	144
Thr	Tyr	Gln	Ala	Ala	Lys	Val	Gly	Val	Asp	Lys	Leu	Ile	Ala	Gly	Val	
		35					40					45				

ccg	gag	ctg	gcc	gac	ctg	gcc	aat	gtg	cgc	ggc	gag	cag	gtg	atg	cag	192
Pro	Glu	Leu	Ala	Asp	Leu	Ala	Asn	Val	Arg	Gly	Glu	Gln	Val	Met	Gln	
	50					55					60					

atc	gcc	tcc	gaa	agc	atc	acc	aac	gac	gac	ctg	ctc	aag	ctg	gca	agc	240
Ile	Ala	Ser	Glu	Ser	Ile	Thr	Asn	Asp	Asp	Leu	Leu	Lys	Leu	Ala	Ser	
65					70					75					80	

agc	gtg	gcc	gag	ctg	gcc	gac	agc	aat	gac	gtc	gat	ggc	atc	gtc	atc	288
Ser	Val	Ala	Glu	Leu	Ala	Asp	Ser	Asn	Asp	Val	Asp	Gly	Ile	Val	Ile	
				85					90						95	
acc	cat	ggc	acc	gac	acc	ctg	gaa	gaa	acc	gcc	tac	ttt	ttg	aac	ctc	336
Thr	His	Gly	Thr	Asp	Thr	Leu	Glu	Glu	Thr	Ala	Tyr	Phe	Leu	Asn	Leu	
			100					105					110			
gtg	gaa	aag	acc	gac	aag	ccg	atc	gtc	gtg	gtc	ggg	tcc	atg	cgc	ccc	384
Val	Glu	Lys	Thr	Asp	Lys	Pro	Ile	Val	Val	Val	Gly	Ser	Met	Arg	Pro	
		115					120					125				
ggc	acc	gcc	atg	tcc	gcc	gac	ggc	atg	ctc	aac	ctg	tac	aac	gcc	gtg	432
Gly	Thr	Ala	Met	Ser	Ala	Asp	Gly	Met	Leu	Asn	Leu	Tyr	Asn	Ala	Val	
	130					135					140					
gcc	gtg	gcc	agc	aac	aag	gac	tcg	cgc	ggc	aag	ggc	gtg	ctg	gtg	acc	480
Ala	Val	Ala	Ser	Asn	Lys	Asp	Ser	Arg	Gly	Lys	Gly	Val	Leu	Val	Thr	
	145				150					155					160	
atg	aac	gac	gag	atc	cag	tcc	ggg	cgt	gac	gtg	agc	aag	tcg	atc	aac	528
Met	Asn	Asp	Glu	Ile	Gln	Ser	Gly	Arg	Asp	Val	Ser	Lys	Ser	Ile	Asn	
				165					170					175		
atc	aag	acc	gaa	gcc	ttc	aag	agc	gcc	tgg	ggc	ccg	ctg	ggc	atg	gtg	576
Ile	Lys	Thr	Glu	Ala	Phe	Lys	Ser	Ala	Trp	Gly	Pro	Leu	Gly	Met	Val	
			180					185					190			
gtg	gaa	ggc	aag	tcg	tac	tgg	ttc	cgc	ctg	ccg	gcc	aag	cgc	cac	acg	624
Val	Glu	Gly	Lys	Ser	Tyr	Trp	Phe	Arg	Leu	Pro	Ala	Lys	Arg	His	Thr	
		195					200					205				
gtc	aac	tcc	gag	ttc	gac	atc	aag	cag	atc	agc	agc	ctg	ccc	cag	gtg	672
Val	Asn	Ser	Glu	Phe	Asp	Ile	Lys	Gln	Ile	Ser	Ser	Leu	Pro	Gln	Val	
	210					215						220				
gac	atc	gcc	tac	agc	tat	ggc	aac	gtc	acc	gac	acg	gcc	tac	aag	gcc	720
Asp	Ile	Ala	Tyr	Ser	Tyr	Gly	Asn	Val	Thr	Asp	Thr	Ala	Tyr	Lys	Ala	
	225				230					235					240	
ctg	gca	cag	aac	ggc	gcc	aag	gcg	ctg	atc	cat	gcc	ggc	acc	ggc	aat	768
Leu	Ala	Gln	Asn	Gly	Ala	Lys	Ala	Leu	Ile	His	Ala	Gly	Thr	Gly	Asn	
			245					250						255		
ggc	tcg	gtg	tcg	tcg	cgg	gtg	gtg	cca	gcc	ctg	cag	gag	ctg	cgc	aag	816
Gly	Ser	Val	Ser	Ser	Arg	Val	Val	Pro	Ala	Leu	Gln	Glu	Leu	Arg	Lys	
			260					265					270			
aac	ggc	gtg	cag	atc	att	cgt	tcg	tca	cgt	caa	cag	ggc	ggg	ttc	gtg	864
Asn	Gly	Val	Gln	Ile	Ile	Arg	Ser	Ser	Arg	Gln	Gln	Gly	Gly	Phe	Val	
		275				280						285				
ctg	cgt	aac	gcc	gag	cag	ccc	gac	gac	aag	aac	gac	tgg	gtc	gtg	gcc	912
Leu	Arg	Asn	Ala	Glu	Gln	Pro	Asp	Asp	Lys	Asn	Asp	Trp	Val	Val	Ala	
	290					295					300					

cac gac ctg aac ccg cag aag gcc cgc atc ctg gcg atg gtg gca atg 960
 His Asp Leu Asn Pro Gln Lys Ala Arg Ile Leu Ala Met Val Ala Met
 305 310 315 320

acc aag acc cag gac agc aag gag ctg cag cgc att ttc tgg gaa tac 1008
 Thr Lys Thr Gln Asp Ser Lys Glu Leu Gln Arg Ile Phe Trp Glu Tyr
 325 330 335

tgataa 1014

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 20 25 30

Thr Tyr Gln Ala Ala Lys Val Gly Val Asp Lys Leu Ile Ala Gly Val
 35 40 45

Pro Glu Leu Ala Asp Leu Ala Asn Val Arg Gly Glu Gln Val Met Gln
 50 55 60

Ile Ala Ser Glu Ser Ile Thr Asn Asp Asp Leu Leu Lys Leu Ala Ser
 65 70 75 80

Ser Val Ala Glu Leu Ala Asp Ser Asn Asp Val Asp Gly Ile Val Ile
 85 90 95

Thr His Gly Thr Asp Thr Leu Glu Glu Thr Ala Tyr Phe Leu Asn Leu
 100 105 110

Val Glu Lys Thr Asp Lys Pro Ile Val Val Val Gly Ser Met Arg Pro
 115 120 125

Gly Thr Ala Met Ser Ala Asp Gly Met Leu Asn Leu Tyr Asn Ala Val
 130 135 140

Ala Val Ala Ser Asn Lys Asp Ser Arg Gly Lys Gly Val Leu Val Thr
 145 150 155 160

Met Asn Asp Glu Ile Gln Ser Gly Arg Asp Val Ser Lys Ser Ile Asn
 165 170 175

Ile Lys Thr Glu Ala Phe Lys Ser Ala Trp Gly Pro Leu Gly Met Val
 180 185 190

Val Glu Gly Lys Ser Tyr Trp Phe Arg Leu Pro Ala Lys Arg His Thr
 195 200 205

Val Asn Ser Glu Phe Asp Ile Lys Gln Ile Ser Ser Leu Pro Gln Val
 210 215 220

Asp Ile Ala Tyr Ser Tyr Gly Asn Val Thr Asp Thr Ala Tyr Lys Ala
 225 230 235 240

Leu Ala Gln Asn Gly Ala Lys Ala Leu Ile His Ala Gly Thr Gly Asn
 245 250 255

Gly Ser Val Ser Ser Arg Val Val Pro Ala Leu Gln Glu Leu Arg Lys
 260 265 270

Asn Gly Val Gln Ile Ile Arg Ser Ser Arg Gln Gln Gly Gly Phe Val
 275 280 285

Leu Arg Asn Ala Glu Gln Pro Asp Asp Lys Asn Asp Trp Val Val Ala
 290 295 300

His Asp Leu Asn Pro Gln Lys Ala Arg Ile Leu Ala Met Val Ala Met
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Thr Lys Thr Gln Asp Ser Lys Glu Leu Gln Arg Ile Phe Trp Glu Tyr
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<210> 4
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<210> 5
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 <212> DNA
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<220>
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<210> 6
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<220>
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<210> 7
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<220>
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<210> 9
 <211> 20
 <212> DNA
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<400> 9
 tgacgatgcc atcgacgtca 20

<210> 10
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20

<210> 11
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<210> 12
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14

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<220>
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<220>
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 tgagcggata acaatttcac acaggaaaca g 91

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 <212> DNA
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<220>
 <223> Description of Artificial Sequence: Synthetic
 promoter

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 tgattaattg tcaacagggg gatggggagt a 91

<210> 21
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 <212> DNA
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<220>
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<220>
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 <222> (46)..(63)

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 Met Lys Glu Val
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gag aac 63
 Glu Asn
 5

<210> 22
 <211> 6
 <212> PRT
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<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 22

Met Lys Glu Val Glu Asn
1 5